

#55, 60

RESULT 7

S38908

glutathione reductase (NADPH) (EC 1.6.4.2) - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 03-Nov-2000

C;Accession: S38908

R;Creissen, G.; Mullineaux, X.Y.Z.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38908

A;Accession: S38908

A;Molecule type: mRNA

A;Residues: 1-557 <CRE>

A;Cross-references: EMBL:X76293; NID:g431954; PIDN:CAA53925.1; PID:g431955

C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology

C;Keywords: FAD; flavoprotein; NADP; oxidoreductase; redox-active disulfide

F;83-528/Domain: dihydrolipoamide dehydrogenase homology <DLD>

F;127-132/Disulfide bonds: redox-active #status predicted

Query Match 27.5%; Score 791.5; DB 2; Length 557;  
Best Local Similarity 38.0%; Pred. No. 1.3e-49;  
Matches 186; Conservative 82; Mismatches 196; Indels 25; Gaps 13;

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Qy      54  NGPEDLPKSYDYDLIIIGGGSGGLAAAKEAAQYGKKVMV--LDFVTPTPLGTRWGLGGTC 111
      || | | : ||: || || || | : : | : | | | : | | : || ||
Db      70  NG-ADAPRHYDFDLFTIGAGSGGVRASRFASNFGASVAVCELPFSTISSDST-GGVGGTC 127

Qy     112  VNVGCIPIPKLMHQAALLGQALQDSRNYGWKVEETVKHWDWMIEAVQNHIGSLNWGYRVA 171
      | ||: || || : | : : || : : | : | : | : | : | : | :
Db     128  VLRGCVPKLLVYASKYSHEFEESCGFGWNYDVEPRFDWSTLIANKNAELQRLTGIYKNI 187

Qy     172  LREKKVYENAYGQFIGPHRIKATNNKGKEKIYSAERFLIATGERPRYLGI PGDKEYCIS 231
      | : | | : : || : | : || | : || | | | | | | | | |
Db     188  LKNAGVTLIEGRGKVVDPHTVDVDG-----KLYSAKNILISVGGRPFIPDIPG-SEY AID 241

Qy     232  SDDLFSLPYCPGKTLVVGASYVALECA GFLAGIGLDVTVMVR-SILLRGFDQDMANKIGE 290
      || | | | | : || | : || | | | | : : | : | : | : | : | : |
Db     242  SDAALDLPTKPNKIAIVGGGYIALEFAGIFNGLKSEVHV FIRQKKVLRGFDEEIRDFVGE 301

Qy     291  HMEEHGIKFIRQFVPIKVEQIEAGTPGRLRVVAQSTNSEEIIIEGEYNTVMLAIGRDACTR 350
      | | ||: | : | : | | : | : | : | : | : | : | : | : |
Db     302  QMSLRGIEFHTEESP---QAIVKSADGSLSL----KTSRGTVEG-FSHIMFATGRRPNTK 353

Qy     351  KIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGRLLAQRLY 410
      : || || || || : | | | : : || | : || || : || || || : | | : :
Db     354  NLGLETVGVKMT-KNGAIEVDEYSRTSVPSIWA VGDV-TDRINLTPVALMEGGALAKTIF 411

Qy     411  AGSTVKCDYENVPTTFTPTPLEYGACGLSEEKAVEKFGEENIEVYHSYFWPLEWTIPSRDN 470
      | | | | || | | : | | | | : || : || : || : | | : | : |
Db     412  AHEPTKPDYRNVPAAVFSQPPIGQVGLMEEQAIKEFGD--VDVYTANFRPLKATISGLPD 469

Qy     471  NKCYAKIICNTKDNERVVG FHVLPNAGEVTQGF AAALKCGLTKKQLDSTIGIHPVCAEV 530
      | : | : | : | : | : | | | | : | | | | | : | : || ||
Db     470  RVFMKLIVC--AKTSKVLGLHMC GDDAPEIVQGFAIAVKAGLTKADFDATVGIHPTS AEE 527

Qy     531  FTTL SVTKR 539
      | | : |

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Db 528 FVTMRTPTR 536